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RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/057,505

TIME: 09:12:36

Input Set : A:\REGEN1260-3.ST25.txt

Output Set: N:\CRF3\02262002\J057505.raw

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2 <110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
3   AURORA BIOSCIENCES CORPORATION
4   TSIEN, Roger
5   HEIM, Roger
6   CUBITT, Andrew
8 <120> TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
10 <130> FILE REFERENCE: REGEN1260-3
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/057,505
C--> 12 <141> CURRENT FILING DATE: 2002-01-25
12 <150> PRIOR APPLICATION NUMBER: US 08/792,553
13 <151> PRIOR FILING DATE: 1997-01-31
15 <150> PRIOR APPLICATION NUMBER: US 09/396,003
16 <151> PRIOR FILING DATE: 1999-09-13
18 <160> NUMBER OF SEQ ID NOS: 31
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 716
24 <212> TYPE: DNA
25 <213> ORGANISM: Aequorea victoria
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(714)
30 <223> OTHER INFORMATION:
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33 atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt      48
34 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
35 1          5          10          15
37 gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag      96
38 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
39          20          25          30
41 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc      144
42 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
43          35          40          45
45 act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc      192
46 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
47          50          55          60
49 tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cgg      240
50 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
51 65          70          75          80
53 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga      288
54 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
55          85          90          95
57 act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc      336

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58 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
59          100          105          110
61 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att      384
62 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
63          115          120          125
65 gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac      432
66 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
67          130          135          140
69 tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga      480
70 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
71 145          150          155          160
73 atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt      528
74 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
75          165          170          175
77 caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct      576
78 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
79          180          185          190
81 gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg      624
82 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
83          195          200          205
85 aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta      672
86 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
87          210          215          220
89 aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa ta      716
90 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
91 225          230          235
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 238
96 <212> TYPE: PRT
97 <213> ORGANISM: Aequorea victoria
99 <400> SEQUENCE: 2
101 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
102 1          5          10          15
105 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
106          20          25          30
109 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
110          35          40          45
113 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
114          50          55          60
117 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
118 65          70          75          80
121 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
122          85          90          95
125 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
126          100          105          110
129 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
130          115          120          125
133 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
134          130          135          140

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137 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
138 145                               150                               155                               160
141 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
142                               165                               170                               175
145 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
146                               180                               185                               190
149 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
150                               195                               200                               205
153 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
154 210                               215                               220
157 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
158 225                               230                               235

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161 <210> SEQ ID NO: 3

162 <211> LENGTH: 8

163 <212> TYPE: PRT

164 <213> ORGANISM: Artificial sequence

166 <220> FEATURE:

167 <223> OTHER INFORMATION: Linker moiety

169 <400> SEQUENCE: 3

171 Ser Gln Asn Tyr Pro Ile Val Gly

172 1 5

175 <210> SEQ ID NO: 4

176 <211> LENGTH: 10

177 <212> TYPE: PRT

178 <213> ORGANISM: Artificial sequence

180 <220> FEATURE:

181 <223> OTHER INFORMATION: Linker moiety

183 <400> SEQUENCE: 4

185 Lys Ala Arg Val Leu Ala Glu Ala Met Ser

186 1 5 10

189 <210> SEQ ID NO: 5

190 <211> LENGTH: 10

191 <212> TYPE: PRT

192 <213> ORGANISM: Artificial sequence

194 <220> FEATURE:

195 <223> OTHER INFORMATION: Linker moiety

197 <400> SEQUENCE: 5

199 Pro Ser Pro Arg Glu Gly Lys Arg Ser Tyr

200 1 5 10

203 <210> SEQ ID NO: 6

204 <211> LENGTH: 5

205 <212> TYPE: PRT

206 <213> ORGANISM: Artificial sequence

208 <220> FEATURE:

209 <223> OTHER INFORMATION: Linker moiety

211 <400> SEQUENCE: 6

213 Tyr Val Ala Asp Gly

214 1 5

217 <210> SEQ ID NO: 7

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218 <211> LENGTH: 8
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Linker moiety
225 <400> SEQUENCE: 7
227 Met Phe Gly Gly Ala Lys Lys Arg
228 1 5
231 <210> SEQ ID NO: 8
232 <211> LENGTH: 10
233 <212> TYPE: PRT
234 <213> ORGANISM: Artificial sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Linker moiety
239 <400> SEQUENCE: 8
241 Gly Val Val Asn Ala Ser Ser Arg Leu Ala
242 1 5 10
245 <210> SEQ ID NO: 9
246 <211> LENGTH: 9
247 <212> TYPE: PRT
248 <213> ORGANISM: Artificial sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Linker moiety
253 <400> SEQUENCE: 9
255 Leu Ile Ala Tyr Leu Lys Lys Ala Thr
256 1 5
259 <210> SEQ ID NO: 10
260 <211> LENGTH: 7
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Linker moiety
267 <400> SEQUENCE: 10
269 Val Lys Met Asp Ala Glu Phe
270 1 5
273 <210> SEQ ID NO: 11
274 <211> LENGTH: 17
275 <212> TYPE: PRT
276 <213> ORGANISM: Artificial sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Linker moiety
281 <400> SEQUENCE: 11
283 Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg
284 1 5 10 15
287 His
291 <210> SEQ ID NO: 12
292 <211> LENGTH: 13
293 <212> TYPE: PRT
294 <213> ORGANISM: Artificial sequence

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296 <220> FEATURE:
297 <223> OTHER INFORMATION: Linker moiety
299 <400> SEQUENCE: 12
301 Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His
302 1      5      10
305 <210> SEQ ID NO: 13
306 <211> LENGTH: 8
307 <212> TYPE: PRT
308 <213> ORGANISM: Artificial sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Linker moiety
313 <400> SEQUENCE: 13
315 Lys Pro Ala Leu Phe Phe Arg Leu
316 1      5
319 <210> SEQ ID NO: 14
320 <211> LENGTH: 30
321 <212> TYPE: PRT
322 <213> ORGANISM: Artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Linker moiety
327 <400> SEQUENCE: 14
329 Gln Pro Leu Gly Gln Thr Ser Leu Met Lys Arg Pro Pro Gly Phe Ser
330 1      5      10      15
333 Pro Phe Arg Ser Val Gln Val Met Lys Thr Gln Glu Gly Ser
334      20      25      30
337 <210> SEQ ID NO: 15
338 <211> LENGTH: 5
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Cleavage recognition sequence
345 <400> SEQUENCE: 15
347 Gly Gly Gly Gly Ser
348 1      5
351 <210> SEQ ID NO: 16
352 <211> LENGTH: 22
353 <212> TYPE: PRT
354 <213> ORGANISM: Artificial sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: Linker moiety
359 <400> SEQUENCE: 16
361 Gly Gly Gly Gly Gly Gly Ser Met Phe Gly Gly Ala Lys Lys Arg Ser
362 1      5      10      15
365 Gly Gly Gly Gly Gly Gly
366      20
369 <210> SEQ ID NO: 17
370 <211> LENGTH: 35
371 <212> TYPE: PRT
372 <213> ORGANISM: Artificial sequence

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VERIFICATION SUMMARY

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Input Set : A:\REGEN1260-3.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date